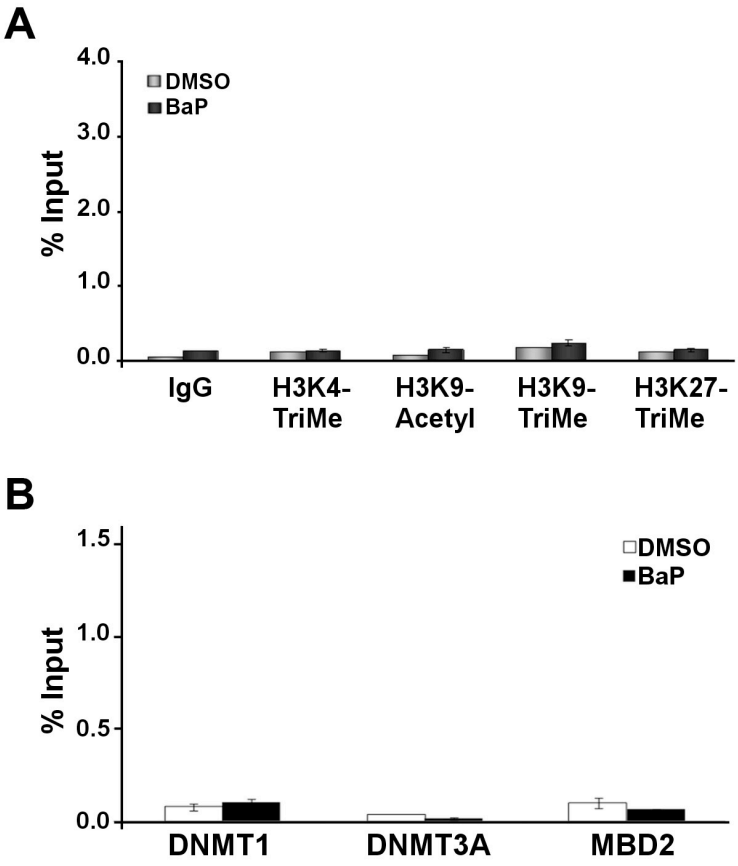
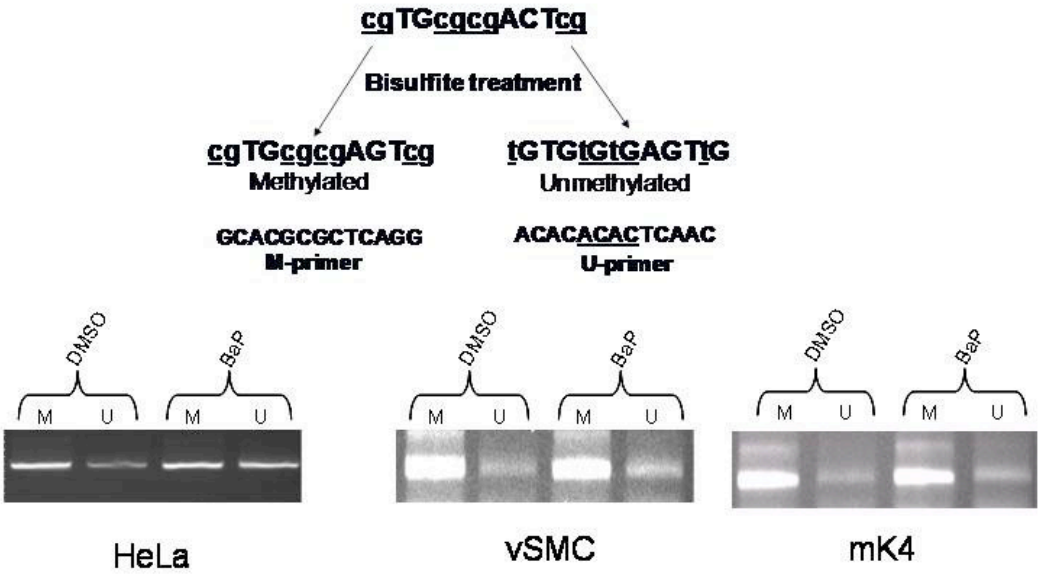
Supplementary Figures



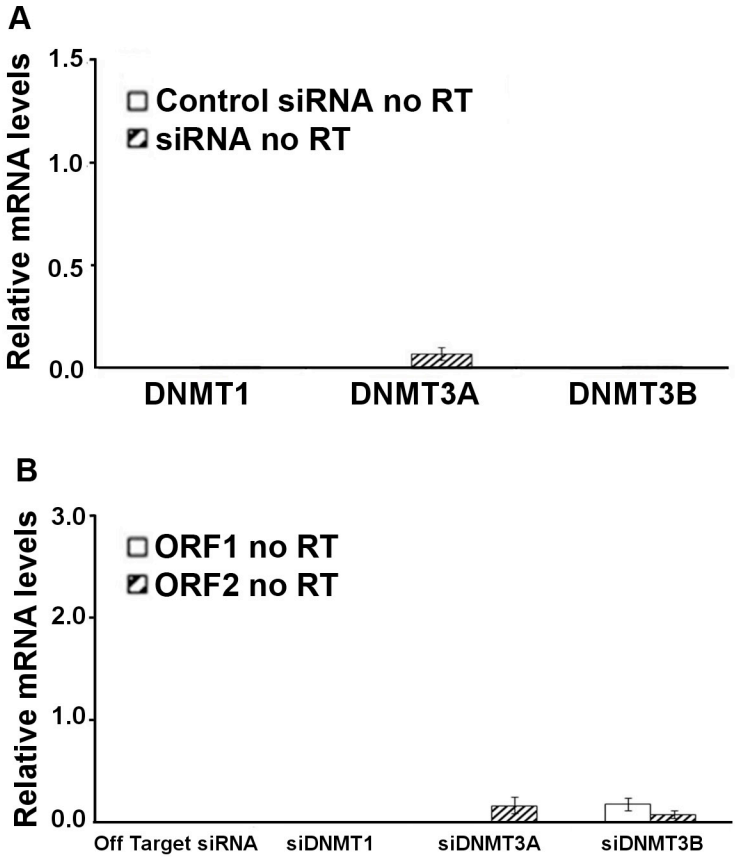
Supplementary Figure 1 – L1 3' UTR is devoid of both histone epigenetic marks and transcription factors. HeLa cells treated with DMSO vehicle or 3 μM BaP for 12 hours were formaldehyde-crosslinked and chromatin processed for ChIP assays. Four μg of antisera were used for each immunoprecipitation with antibodies targeting different histone modifications or transcription factors as shown and purified DNA subjected to real time PCR. (a) and (b): Real time PCR for DNA samples from ChIP assays with the indicated antibodies was performed using primers targeting the L1 3'UTR region. Isotype-matched IgG control for all reactions is shown in (a). The results shown are representative of experiments performed in triplicate for each sample and repeated 3 separate times. Calculations for L1 promoter sequence enrichment within ChIP samples was performed according to the SABiosciences ChIP-qPCR Data Analysis

manual (http://www.sabiosciences.com/chipqpcrresource.php) and plotted as a function of percent enrichment relative to input (% input) chromatin. Statistic analyses done using ANOVA (*indicate statistically significant differences, $p<0.05$).



Supplementary Figure 2. BaP causes hypomethylation of the human and mouse L1 promoters.

Allele-specific methylation PCR (MS-PCR) targeting multiple CpG sites on the human and mouse L1 promoters. Primers specific for methylated (M) or unmethylated (U) DNA were used to amplify DNA from BaP treated cells (upper panel). BaP treatment increases unmethylated signal (U) in both human cervical cancer cells (HeLa) and mouse primary aortic vascular smooth muscle cells (vSMC) and mouse late embryonic mesenchymal epithelial cells (MK4), indicating local hypomethylation of the L1 5'UTR.



Supplementary Figure 3. RNA samples from siRNA transfected cells are devoid of genomic DNA contaminants. HeLa cells were transfected with 50 nM siRNA control (off target) or siRNA targeting DNMT1, DNMT3A or DNMT3B. RNA was extracted 48 hours after initial plating of the cells. cDNA synthesis reactions were carried out in the absence of reverse transcriptase. (a): Real time PCR results using PCR primers for amplification of the indicated DNMTs. (b): Real time PCR results using PCR primers for amplification of L1 ORF1 and ORF2. For all experiments relative quantitative analyses were done using the Livak method of ΔΔCt, and statistic analyses were done using ANOVA (* indicates statistically significant differences, $p<0.05$). Each experiment was run with 3 replicates and repeated at least 2X.